

WEST Search History

DATE: Thursday, February 22, 2007

Hide?	Set Name	Query	Hit Count
	<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=NO; OP=OR</i>		
<input type="checkbox"/>	L21	l10 and l17	20
<input type="checkbox"/>	L20	L10 and l13	2
<input type="checkbox"/>	L19	l10 and l14	7
<input type="checkbox"/>	L18	l10 and l11	2
<input type="checkbox"/>	L17	freund\$ adj3 adjuvant	28946
<input type="checkbox"/>	L16	freund\$ adj5 adjuvant	28980
<input type="checkbox"/>	L15	odn	2565
<input type="checkbox"/>	L14	cpG	11794
<input type="checkbox"/>	L13	human adj growth adj hormone or hgh	17274
<input type="checkbox"/>	L12	polycationic adj3 peptide	143
<input type="checkbox"/>	L11	polycationic adj5 polymer	893
<input type="checkbox"/>	L10	l7 and L8	80
<input type="checkbox"/>	L9	l7 and l8L8	0
<input type="checkbox"/>	L8	sera or serum	232417
<input type="checkbox"/>	L7	l5 and l6	80
<input type="checkbox"/>	L6	hyperimmune or hyper-immune	2507
<input type="checkbox"/>	L5	l3 and L4	439
<input type="checkbox"/>	L4	vaccine	59965
<input type="checkbox"/>	L3	l1 and L2	794
<input type="checkbox"/>	L2	antigen or antigens	167562
<input type="checkbox"/>	L1	chlamydia adj pneumoniae	1351

END OF SEARCH HISTORY



results of BLAST

TBLASTN 2.2.15 [Oct-15-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1172167648-4382-68418259592.BLASTQ2

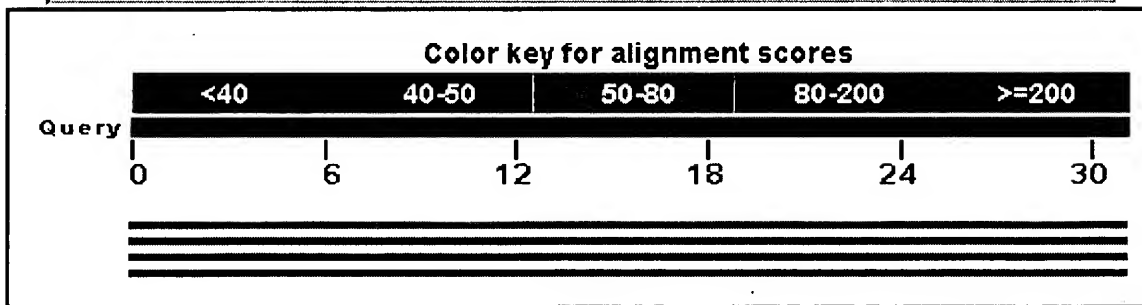
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
5,005,800 sequences; 19,835,896,028 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=31

Distribution of 4 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



Sequences producing significant alignments:	Score (Bits)	E Value
gi 33236121 gb AE017158.1 Chlamydophila pneumoniae TW-183, s...	63.2	2e-08
gi 12057210 gb AE002161.1 Chlamydophila pneumoniae AR39, comple	63.2	2e-08
gi 6626250 gb AE001363.1 Chlamydophila pneumoniae CWL029, compl	63.2	2e-08
gi 47118320 dbj BA000008.3 Chlamydophila pneumoniae J138 genomi	63.2	2e-08

Alignments

Get selected sequences

Select all

Deselect all

W022002

> ☐ gi|33236121|gb|AE017158.1| ☒ Chlamydomophila pneumoniae TW-183, section 2 of 4 of genome
Length=300380

Features in this part of subject sequence:
hypothetical protein

Score = 63.2 bits (152), Expect = 2e-08
Identities = 31/31 (100%), Positives = 31/31 (100%), Gaps = 0/31 (0%)
Frame = +1

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RVMKAVVSHKSRTSSIHRQYSSYSYSLFYSLK
Sbjct 260287 RVMKAVVSHKSRTSSIHRQYSSYSYSLFYSLK 260379

> ☐ gi|12057210|gb|AE002161.1| ☒ Chlamydomophila pneumoniae AR39, complete genome
Length=1229853

Features in this part of subject sequence:
hypothetical protein

Score = 63.2 bits (152), Expect = 2e-08
Identities = 31/31 (100%), Positives = 31/31 (100%), Gaps = 0/31 (0%)
Frame = -2

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Sbjct 277757 RVMKAVVSHKSRTSSIHRQYSSYSYSLFYSLK 277665

> ☐ gi|6626250|gb|AE001363.1| ☒ Chlamydomophila pneumoniae CWL029, complete genome
Length=1230230

Features in this part of subject sequence:
hypothetical protein

Score = 63.2 bits (152), Expect = 2e-08
Identities = 31/31 (100%), Positives = 31/31 (100%), Gaps = 0/31 (0%)
Frame = +3

Query 1 RVMKAVVSHKSRTSSIHRQYSSYSYSLFYSLK 31
RVMKAVVSHKSRTSSIHRQYSSYSYSLFYSLK
Sbjct 563829 RVMKAVVSHKSRTSSIHRQYSSYSYSLFYSLK 563921

> ☐ gi|47118320|dbj|BA000008.3| ☒ Chlamydomophila pneumoniae J138 genomic DNA, complet
Length=1226565

Features in this part of subject sequence:
hypothetical protein

Score = 63.2 bits (152), Expect = 2e-08
Identities = 31/31 (100%), Positives = 31/31 (100%), Gaps = 0/31 (0%)
Frame = +3

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RVMKAVVSHKSRTSSIHRQYSSYSYSLFYSLK
Sbjct 563148 RVMKAVVSHKSRTSSIHRQYSSYSYSLFYSLK 563240

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Feb 21, 2007 5:53 PM

Number of letters in database: -1,638,940,448

Number of sequences in database: 5,005,800

Lambda	K	H
0.321	0.124	0.329

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 5005800

Number of Hits to DB: 59870585

Number of extensions: 300715

Number of successful extensions: 2818

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 2818

Number of HSP's successfully gapped: 0

Length of query: 31

Length of database: 19835896028

Length adjustment: 6

Effective length of query: 25

Effective length of database: 6581930542

Effective search space: 164548263550

Effective search space used: 164548263550

T: 13

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 40 (20.0 bits)

S2: 77 (34.3 bits)




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Display Show Hide: ☐ sequence ☐ all but gene, CDS and mRNA

Range: from to ☐ Reverse complemented strand

☐ 1: [AE017158](#). Reports *Chlamydomonada* pne...[gi:33236121]

[Links](#)

[Features](#) [Sequence](#)

LOCUS AE017158 3102 bp DNA linear BCT 25-JUL-2003
 DEFINITION *Chlamydomonada pneumoniae* TW-183, section 2 of 4 of the complete genome.
 ACCESSION [AE017158](#) REGION: 258324..261425
 VERSION AE017158.1 GI:33236121
 KEYWORDS
 SOURCE *Chlamydomonada pneumoniae* TW-183
 ORGANISM *Chlamydomonada pneumoniae* TW-183
 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomonada.
 REFERENCE 1 (bases 1 to 3102)
 AUTHORS Geng,M.M., Schuhmacher,A., Muehldorfer,I., Bensch,K.W., Schaefer,K.P., Schneider,S., Pohl,T., Essig,A., Marre,R. and Melchers,K.
 TITLE The genome sequence of *Chlamydia pneumoniae* TW183 and comparison with other *Chlamydia* strains based on whole genome sequence analysis
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3102)
 AUTHORS Geng,M.M., Schuhmacher,A., Muehldorfer,I., Bensch,K.W., Schaefer,K.P., Schneider,S., Pohl,T. and Melchers,K.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAY-2002) RDR/IT, RDR/FG, RDR/BT, ALTANA Pharma, Byk-Gulden-Str. 2, Konstanz 78467, Germany
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 SNP"

ORIGIN

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3061 actgaagatc agaactcaaa accggacagc tcaaatccct ag

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NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Display Show Send to Hide: ☐ sequence ☐ all but gene, CDS and mRN

Range: from to ☐ Reverse complemented str

☐ 1: [AE001363](#). Reports *Chlamydomonada p...* [gi:6626250]

[Links](#)

[Comment](#) [Features](#) [Sequence](#)

LOCUS AE001363 3132 bp DNA linear BCT 26-JAN-2006
DEFINITION *Chlamydomonada pneumoniae* CWL029, complete genome.
ACCESSION [AE001363](#) REGION: 561836..564967
VERSION AE001363.1 GI:6626250
KEYWORDS
SOURCE *Chlamydomonada pneumoniae* CWL029
ORGANISM *Chlamydomonada pneumoniae* CWL029
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomonada.
REFERENCE 1 (bases 1 to 3132)
AUTHORS Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W.,
Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
TITLE Comparative genomes of *Chlamydomonada pneumoniae* and *C. trachomatis*
JOURNAL Nat. Genet. 21 (4), 385-389 (1999)
PUBMED 10192388
REFERENCE 2 (bases 1 to 3132)
AUTHORS Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Olinger,L.,
Grimwood,J., Davis,R.W. and Stephens,R.S.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1998) Program in Infectious Diseases, University
of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
COMMENT On or before Jan 26, 2006 this sequence version replaced
[gi:4376255](#), [gi:4376263](#), [gi:4376271](#), [gi:4376277](#), [gi:4376288](#),
[gi:4376299](#), [gi:4376311](#), [gi:4376322](#), [gi:4376334](#), [gi:4376341](#),
[gi:4376353](#), [gi:4376357](#), [gi:4376367](#), [gi:4376375](#), [gi:4376387](#),
[gi:4376398](#), [gi:4376409](#), [gi:4376416](#), [gi:4376422](#), [gi:4376438](#),
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[gi:4376515](#), [gi:4376529](#), [gi:4376541](#), [gi:4376550](#), [gi:4376562](#),
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[gi:4377378](#), [gi:4377389](#), [gi:4377398](#).

FEATURES Location/Qualifiers


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ORIGIN

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Display Show Hide: ☐ sequence ☐ all but gene, CDS and mRNA

Range: from to ☐ Reverse complemented strand

☐ 1: [BA000008](#). Reports *Chlamydomonas reinhardtii* [gi:47118320]

[Links](#)

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DEFINITION *Chlamydomonas reinhardtii* J138 genomic DNA, complete sequence.
ACCESSION [BA000008](#) REGION: 561155..564286
VERSION BA000008.3 GI:47118320
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ORGANISM *Chlamydomonas reinhardtii* J138
 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomonas.
REFERENCE 1
AUTHORS Shirai,M., Hirakawa,H., Ouchi,K., Tabuchi,M., Kishi,F., Kimoto,M., Takeuchi,H., Nishida,J., Shibata,K., Fujinaga,R., Yoneda,H., Matsushima,H., Tanaka,C., Furukawa,S., Miura,K., Nakazawa,A., Ishii,K., Shiba,T., Hattori,M., Kuhara,S. and Nakazawa,T.
TITLE Comparison of outer membrane protein genes omp and pmp in the whole genome sequences of *Chlamydomonas reinhardtii* isolates from Japan and the United States
JOURNAL J. Infect. Dis. 181 SUPPL 3, S524-S527 (2000)
PUBMED [10839753](#)
REFERENCE 2
AUTHORS Shirai,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Ouchi,K., Shiba,T., Ishii,K., Hattori,M., Kuhara,S. and Nakazawa,T.
TITLE Comparison of whole genome sequences of *Chlamydomonas reinhardtii* J138 from Japan and CWL029 from USA
JOURNAL Nucleic Acids Res. 28 (12), 2311-2314 (2000)
PUBMED [10871362](#)
REFERENCE 3 (bases 1 to 3132)
AUTHORS Hattori,M., Ishii,K. and Shiba,T.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-2000) Masahira Hattori, Kitasato Institute for Life Sciences, Kitasato University; Kitasato 1-15-1, Sagami-hara, Kanagawa 228-8555, Japan
 (E-mail:hattori@genome.ls.kitasato-u.ac.jp,
 URL:http://genome.ls.kitasato-u.ac.jp/, Tel:81-42-778-8194,
 Fax:81-42-778-8193)
COMMENT On or before Nov 5, 2004 this sequence version replaced gi:9956082, gi:10176692, gi:10176693, gi:10176694.
 This work was done in collaboration with Mutsunori Shirai, Mitsuaki Kimoto, Mitsuaki Tabuchi, Fumio Kishi, Teruko Nakazawa (Yamaguchi University), Kazunobu Ouchi (Shimonoseki Saiseikai General Hospital), Hideki Hirakawa, Satoru Kuhara (Kuyshu University), and supported by the Research for the Future Program of the Japan Society for the Promotion of Science.
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☐ 1: [AAF38131](#). Reports hypothetical prot...[gi:7189196]

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 VERSION AAF38131.1 GI:7189196
 DBSOURCE accession [AE002161.1](#)
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 ORGANISM [Chlamydophila pneumoniae AR39](#)
 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
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 AUTHORS Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,
 White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T.,
 Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
 Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J.,
 McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
 TITLE Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 pneumoniae AR39
 JOURNAL Nucleic Acids Res. 28 (6), 1397-1406 (2000)
 PUBMED [10684935](#)
 REFERENCE 2 (residues 1 to 1033)
 AUTHORS Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,
 White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T.,
 Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
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 McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
 TITLE Direct Submission
 JOURNAL Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA
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Entrez

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information for
human, fruit fly,
mouse, rat, and
zebrafish

GI	Version	Update Date	Status	I	II
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7189196	1	Jun 1 2000 6:51 PM	Dead		
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Accession AAF38131 was first seen at NCBI on Mar 7 2000 11:02 AM

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NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Display Show Hide: ☐ sequence ☐ all but gene, CDS and mRNA

Range: from to ☐ Reverse complemented str

☐ 1: [AE002161](#). Reports *Chlamydomphila pne...*[gi:12057210]

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DEFINITION *Chlamydomphila pneumoniae* AR39, complete genome.
ACCESSION [AE002161](#) REGION: 276619..279720
VERSION AE002161.1 GI:12057210
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ORGANISM *Chlamydomphila pneumoniae* AR39
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomphila.
REFERENCE 1 (bases 1 to 3102)
AUTHORS Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
TITLE Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39
JOURNAL Nucleic Acids Res. 28 (6), 1397-1406 (2000)
PUBMED [10684935](#)
REFERENCE 2 (bases 1 to 3102)
AUTHORS Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
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FEATURES

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